



PALM INTRANET

Day : Sunday  
Date: 3/6/2005  
Time: 07:02:12

# Continuity Information for 09/259389

## Parent Data

09259389Claims Priority from Provisional Application 60076325

## Child Data

No Child Data

Appln Info

Contents

Petition Info

Atty/Agent Info

Continuity  
Data

Foreign Data

Invent

Search Another: Application# 

Search

or Patent# 

Search

PCT /  / 

Search

or PG PUBS # 

Search

Attorney Docket # 

Search

Bar Code # 

Search

To go back use Back button on your browser toolbar.

Back to [PALM](#) | [ASSIGNMENT](#) | [OASIS](#) | [Home page](#)

**PALM INTRANET**Day : Sunday  
Date: 3/6/2005  
Time: 07:02:18

## Inventor Information for 09/259389

Inventor Name	City	State/Country
GEORGOPOULOS, KATIA	LEXINGTON	MASSACHUSETTS
MORGAN, BRUCE A.	LEXINGTON	MASSACHUSETTS
KELLY, CLAIR	BOSTON	MASSACHUSETTS

[Appln Info](#)[Contents](#)[Petition Info](#)[Atty/Agent Info](#)[Continuity Data](#)[Foreign Data](#)Search Another: Application#   or Patent#  PCT /  /   or PG PUBS #  Attorney Docket #  Bar Code #  

To go back use Back button on your browser toolbar.

Back to [PALM](#) | [ASSIGNMENT](#) | [OASIS](#) | [Home page](#)

agc agg gaa aca tct gat agt cac gaa aac aac atg gat ggc ccc atc	1152
Ser Arg Glu Thr Ser Asp Ser His Glu Asn Asn Met Asp Gly Pro Ile	
370 375 380	
tct ctc atc aga cca aag agt cga ccc cag gaa aga gag gcc tcg ccc	1200
Ser Leu Ile Arg Pro Lys Ser Arg Pro Gln Glu Arg Glu Ala Ser Pro	
385 390 395 400	
agc aat agc tgc ctc gat tct act gac tca gaa agt agc cat gat gac	1248
Ser Asn Ser Cys Leu Asp Ser Thr Asp Ser Glu Ser Ser His Asp Asp	
405 410 415	
cgc cag tcc tac caa gga aac cct gcc tta aat ccc aag agg aaa caa	1296
Arg Gln Ser Tyr Gln Gly Asn Pro Ala Leu Asn Pro Lys Arg Lys Gln	
420 425 430	
agc cca gct tac atg aag gag gat gtc aag gct ttg gat gct acc aag	1344
Ser Pro Ala Tyr Met Lys Glu Asp Val Lys Ala Leu Asp Ala Thr Lys	
435 440 445	
gcc ccc aag ggc tct ctg aag gac atc tat aag gtt ttc aat gga gaa	1392
Ala Pro Lys Gly Ser Leu Lys Asp Ile Tyr Lys Val Phe Asn Gly Glu	
450 455 460	
gga gaa cag ata agg gcc ttc aag tgt gag cac tgc cga gtc ctt ttt	1440
Gly Glu Gln Ile Arg Ala Phe Lys Cys Glu His Cys Arg Val Leu Phe	
465 470 475 480	
cta gac cat gtc atg tac acc att cac atg ggt tgc cat ggc tac cgg	1488
Leu Asp His Val Met Tyr Thr Ile His Met Gly Cys His Gly Tyr Arg	
485 490 495	
gac cca ctg gaa tgc aac atc tgt ggc tac aga agc cag gac cgc tac	1536
Asp Pro Leu Glu Cys Asn Ile Cys Gly Tyr Arg Ser Gln Asp Arg Tyr	
500 505 510	
gaa ttt tca tca cac att gtt ggg ggg cag cac aca ttc cac	1578
Glu Phe Ser Ser His Ile Val Gly Gly Gln His Thr Phe His	
515 520 525	
taggcgtttg cattccaagg	1598

<210> 2  
 <211> 526  
 <212> PRT  
 <213> Mus musculus

<400> 2  
 Met Glu Thr Asp Ala Ile Asp Gly Tyr Ile Thr Cys Asp Asn Glu Leu  
 1 5 10 15  
 Ser Pro Glu Gly Glu His Ala Asn Met Ala Ile Asp Leu Thr Ser Ser  
 20 25 30  
 Thr Pro Asn Gly Gln His Ala Ser Pro Ser His Met Thr Ser Thr Asn  
 35 40 45  
 Ser Val Lys Leu Glu Met Gln Ser Asp Glu Glu Cys Asp Arg Gln Pro  
 50 55 60  
 Leu Ser Arg Glu Asp Glu Ile Arg Gly His Asp Glu Gly Ser Ser Leu  
 65 70 75 80  
 Glu Glu Pro Leu Ile Glu Ser Ser Glu Val Ala Asp Asn Arg Lys Val  
 85 90 95  
 Gln Asp Leu Gln Gly Glu Gly Gly Ile Arg Leu Pro Asn Gly Lys Leu  
 100 105 110

aga agc cag gac cgc tac gaa ttt tca tca cac att gtt ggg ggg cag	1488
Arg Ser Gln Asp Arg Tyr Glu Phe S r Ser His Ile Val Gly Gly Gln	
485 490 495	

cac aca ttc cac taggcggttg cattccaagg	1520
His Thr Phe His	
500	

<210> 4  
 <211> 500  
 <212> PRT  
 <213> Mus musculus

<400> 4

Met	Glu	Thr	Asp	Ala	Ile	Asp	Gly	Tyr	Ile	Thr	Cys	Asp	Asn	Glu	Leu
1				5				10						15	
Ser	Pro	Glu	Gly	Glu	His	Ala	Asn	Met	Ala	Ile	Asp	Leu	Thr	Ser	Ser
		20					25						30		
Thr	Pro	Asn	Gly	Gln	His	Ala	Ser	Pro	Ser	His	Met	Thr	Ser	Thr	Asn
		35					40					45			
Ser	Val	Lys	Leu	Glu	Met	Gln	Ser	Asp	Glu	Glu	Cys	Asp	Arg	Gln	Pro
	50					55					60				
Leu	Ser	Arg	Glu	Asp	Glu	Ile	Arg	Gly	His	Asp	Glu	Gly	Ser	Ser	Leu
65					70					75					80
Glu	Glu	Pro	Leu	Ile	Glu	Ser	Ser	Glu	Val	Ala	Asp	Asn	Arg	Lys	Val
				85					90					95	
Gln	Asp	Leu	Gln	Gly	Glu	Gly	Gly	Ile	Arg	Leu	Pro	Asn	Gly	Glu	Arg
			100					105					110		
Pro	Phe	His	Cys	Asn	Gln	Cys	Gly	Ala	Ser	Phe	Thr	Gln	Lys	Gly	Asn
	115						120					125			
Leu	Leu	Arg	His	Ile	Lys	Leu	His	Ser	Gly	Glu	Lys	Pro	Phe	Lys	Cys
	130					135					140				
Pro	Phe	Cys	Ser	Tyr	Ala	Cys	Arg	Arg	Arg	Asp	Ala	Leu	Thr	Gly	His
145					150					155					160
Leu	Arg	Thr	His	Ser	Val	Gly	Lys	Pro	His	Lys	Cys	Asn	Tyr	Cys	Gly
				165					170					175	
Arg	Ser	Tyr	Lys	Gln	Arg	Thr	Ser	Leu	Glu	Glu	His	Lys	Glu	Arg	Cys
			180					185						190	
His	Asn	Tyr	Leu	Gln	Asn	Val	Ser	Met	Glu	Ala	Ala	Gly	Gln	Val	Met
	195						200					205			
Ser	His	His	Val	Pro	Pro	Met	Glu	Asp	Cys	Lys	Glu	Gln	Glu	Pro	Ile
	210					215					220				
Met	Asp	Asn	Asn	Ile	Ser	Leu	Val	Pro	Phe	Glu	Arg	Pro	Ala	Val	Ile
225					230					235					240
Glu	Lys	Leu	Thr	Ala	Asn	Met	Gly	Lys	Arg	Lys	Ser	Ser	Thr	Pro	Gln
				245					250					255	
Lys	Phe	Val	Gly	Glu	Lys	Leu	Met	Arg	Phe	Ser	Tyr	Pro	Asp	Ile	His
			260					265					270		
Phe	Asp	Met	Asn	Leu	Thr	Tyr	Glu	Lys	Glu	Ala	Glu	Leu	Met	Gln	Ser
		275					280					285			
His	Met	Met	Asp	Gln	Ala	Ile	Asn	Asn	Ala	Ile	Thr	Tyr	Leu	Gly	Ala
	290					295					300				
Glu	Ala	Leu	His	Pro	Leu	Met	Gln	His	Ala	Pro	Ser	Thr	Ile	Ala	Glu
305					310					315					320
Val	Ala	Pro	Val	Ile	Ser	Ser	Ala	Tyr	Ser	Gln	Val	Tyr	His	Pro	Asn
				325					330					335	
Arg	Ile	Glu	Arg	Pro	Ile	Ser	Arg	Glu	Thr	Ser	Asp	Ser	His	Glu	Asn
			340					345					350		
Asn	Met	Asp	Gly	Pro	Ile	Ser	Leu	Ile	Arg	Pro	Lys	Ser	Arg	Pro	Gln
		355					360						365		

ata agc tca gct tat tct cag gtc tat cat cca aat agg ata gaa aga	1287
Ile Ser Ser Ala Tyr Ser Gln Val Tyr His Pro Asn Arg Ile Glu Arg	
355 360 365	
ccc att agc agg gaa act gct gat agt cat gaa aac aac atg gat ggc	1335
Pro Ile Ser Arg Glu Thr Ala Asp Ser His Glu Asn Asn Met Asp Gly	
370 375 380	
ccc atc tct ctc atc aga cca aag agt cga ccc cag gaa aga gag gcc	1383
Pro Ile Ser Leu Ile Arg Pro Lys Ser Arg Pro Gln Glu Arg Glu Ala	
385 390 395	
tct ccc agc aat agc tgc ctg gat tcc act gac tca gaa agc agc cat	1431
Ser Pro Ser Asn Ser Cys Leu Asp Ser Thr Asp Ser Glu Ser Ser His	
400 405 410	
gat gac cac cag tcc tac caa gga cac cct gcc tta aat ccc aag agg	1479
Asp Asp His Gln Ser Tyr Gln Gly His Pro Ala Leu Asn Pro Lys Arg	
415 420 425 430	
aaa caa agc cca gct tac atg aag gag gat gtc aaa gct ttg gat act	1527
Lys Gln Ser Pro Ala Tyr Met Lys Glu Asp Val Lys Ala Leu Asp Thr	
435 440 445	
acc aag gct cct aag ggc tct ctg aag gac atc tac aag gtc ttc aat	1575
Thr Lys Ala Pro Lys Gly Ser Leu Lys Asp Ile Tyr Lys Val Phe Asn	
450 455 460	
ggg gaa gga gaa cag att agg gcc ttc aag tgt gag cac tgc cga gtc	1623
Gly Glu Gly Glu Gln Ile Arg Ala Phe Lys Cys Glu His Cys Arg Val	
465 470 475	
ctt ttc cta gac cat gtc atg tac acc att cac atg ggt tgc cat ggc	1671
Leu Phe Leu Asp His Val Met Tyr Thr Ile His Met Gly Cys His Gly	
480 485 490	
tac cgg gac cca ctg gaa tgt aac atc tgt ggc tac aga agc cag gac	1719
Tyr Arg Asp Pro Leu Glu Cys Asn Ile Cys Gly Tyr Arg Ser Gln Asp	
495 500 505 510	
cgt tat gag ttt tca tca cac att gtt cga ggg gag cac aca ttc cac	1767
Arg Tyr Glu Phe Ser Ser His Ile Val Arg Gly Glu His Thr Phe His	
515 520 525	
taggcctttt cattccaaag gggaccctat gaagtaaaga ctgcacatga agaaatactg	1827
cacttacaat cccacctttc ctcaaagtgt gtacctttta tttttttaat ataatactgg	1887
tgataatctt attttgtgga gcagtgatcat ttgctctgct	1927

<210> 6  
 <211> 526  
 <212> PRT  
 <213> Homo sapiens

<400> 6  
 Met Glu Thr Glu Ala Ile Asp Gly Tyr Ile Thr Cys Asp Asn Glu Leu  
 1 5 10 15  
 Ser Pro Glu Arg Glu His Ser Asn Met Ala Ile Asp Leu Thr Ser Ser  
 20 25 30  
 Thr Pro Asn Gly Gln His Ala Ser Pro Ser His Met Thr Ser Thr Asp  
 35 40 45  
 Ser Val Lys Leu Glu Met Gln Ser Asp Glu Glu Cys Asp Arg Lys Pro  
 50 55 60